Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for ~~preventing or~~ treating HIV infection in a human caused by a ~~macrophage tropic strain~~ of HIV, wherein HIV entry into an immune cell is facilitated by a CCR5 receptor ~~in a human~~, said method comprising:

a) transplanting into the human a stem cell-rich population of cells from a human donor, wherein the stem cell-rich population of cells has a beneficial gene that is a homozygous polymorphism in a CCR5 gene and the encoded CCR5 receptor does not facilitate HIV entry into the immune cell, thereby preventing or treating said HIV infection, and wherein the stem cell-rich population of cells is umbilical cord blood.

2-14. (Cancelled)

15. (Previously presented) The method of claim 1, wherein said polymorphism is a 32 basepair deletion in the coding region.

16. (Previously presented) The method of claim 1, wherein said polymorphism is CCR5m303.

17. (Previously presented) The method of claim 1, wherein said polymorphism is in the promoter region of CCR5.

18-19. (Cancelled)

20. (Previously presented) The method of claim 1, wherein said method further comprises identification of the HLA genotype or phenotype of said stem cell-rich population of cells.

21-23. (Cancelled)

24. (Previously presented) The method of claim 1, further comprising a step of screening a cell sample from a human donor to identify the stem cell-rich population of cells that has a polymorphism in the CCR5 gene.

25. (Previously presented) The method of claim 24, wherein said polymorphism in the CCR5 gene is detected using a hybridization-based assay, a sequencing assay, or a functional assay.

26-27. (Cancelled)

28. (Previously presented) The method of claim 24, wherein said method further comprises

b) identification of an HLA genotype or phenotype of said stem cell-rich population of cells.

29. (Previously presented) The method of claim 28, wherein said identification of the HLA genotype is via a high-throughput method using allele-specific primers and HLA locus-specific capture oligonucleotides immobilized on a solid phase.

30. (Previously presented) The method of claim 28, wherein said method further comprises

c) identification of an HLA genotype or phenotype of said human.

31. (Previously presented) The method of claim 28, wherein said HLA genotype or phenotype of said stem cell-rich population of cells is compatible with said HLA genotype or phenotype of said human.

32. (Cancelled)

33. (Currently amended) The method of ~~claims 1 or 32~~ claim 1, wherein multiple samples of the stem cell-rich populations of cells with the beneficial gene are transplanted into the human.

34. (Previously presented) The method of claim 33, wherein the multiple samples of the stem cell-rich populations of cells with the beneficial gene have an HLA unmatched genotype or phenotype.